08/478153

Partial Sequence of the Crystal Protein Gene

```
AAGTGGATTTTTATATATAAGTATAAAAAGTAATAAGACTTTAAAATAAGTTAACGGAATACAAACCCTTAATGCATTGGTTAAACATTGTAAAGTCTAAA
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+  100

CCATGCATAATGGGCCAGAAGTAAGTAGATTGTTAACACCCTGGGTCAAAAATTGATATTTAGTAAAATTAGTTGCACTTTGTGCATTTTTTGATAAGAT
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+  200

GAGTCATATGTTTTAAATTGTAGTAATGAAAAACAGTATTATATCATAATGAATTGGTATCTTAATAAAAGAGATGGAGGTAACTTATGGATAACAATCC
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+  300
                                                                                       MetAspAsnAsnPr

GAACATCAATGAATGCATTCCTTATAATTGTTTAAGTAACCCTGAAGTAGAAGTATTAGGTGGAGAAAGAATAGAAACTGGTTACACCCCAATCGATATT
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+  400
oAsnIleAsnGluCysIleProTyrAsnCysLeuSerAsnProGluValGluValLeuGlyGlyGluArgIleGluThrGlyTyrThrProIleAspIle

TCCTTGTCGCTAACGCAATTTCTTTTGAGTGAATTTGTTCCCGGTGCTGGATTTGTGTTAGGACTAGTTGATATAATATGGGGAATTTTTGGTCCCTCTC
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+  500
SerLeuSerLeuThrGlnPheLeuLeuSerGluPheValProGlyAlaGlyPheValLeuGlyLeuValAspIleIleTrpGlyIlePheGlyProSerG

AATGGGACGCATTTCTTGTACAAATTGAACAGTTAATTAACCAAAGAATAGAAGAATTCGCTAGGAACCAAGCCATTTCTAGATTAGAAGGACTAAGCAA
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+  600
lnTrpAspAlaPheLeuValGlnIleGluGlnLeuIleAsnGlnArgIleGluGluPheAlaArgAsnGlnAlaIleSerArgLeuGluGlyLeuSerAs

TCTTTATCAAATTTACGCAGAATCTTTTAGAGAGTGGGAAGCAGATCCTACTAATCCAGCATTAAGAGAAGAGATGCGTATTCAATTCAATGACATGAAC
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+  700
nLeuTyrGlnIleTyrAlaGluSerPheArgGluTrpGluAlaAspProThrAsnProAlaLeuArgGluGluMetArgIleGlnPheAsnAspMetAsn

AGTGCCCTTACAACCGCTATTCCTCTTTTTGCAGTTCAAAATTATCAAGTTCCTCTTTTATCAGTATATGTTCAAGCTGCAAATTTACATTTATCAGTTT
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+  800
SerAlaLeuThrThrAlaIleProLeuPheAlaValGlnAsnTyrGlnValProLeuLeuSerValTyrValGlnAlaAlaAsnLeuHisLeuSerValL

TGAGAGATGTTTCAGTGTTTGGACAAAGGTGGGGATTTGATGCCGCGACTAGCAATAGTCGTTATAATGATTTAACTAGGCTTATTGGCAACTATACAGA
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+  900
euArgAspValSerValPheGlyGlnArgTrpGlyPheAspAlaAlaThrSerAsnSerArgTyrAsnAspLeuThrArgLeuIleGlyAsnTyrThrAs

TTATGCTGTACGCTGGTACAATACGGGATTAGAACGTGTATGGGGACCGGATTCTAGAGATTGGGTAAGGTATAATCAATTTAGAAGAGAATTAACACTA
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+  1000
pTyrAlaValArgTrpTyrAsnThrGlyLeuGluArgValTrpGlyProAspSerArgAspTrpValArgTyrAsnGlnPheArgArgGluLeuThrLeu

ACTGTATTAGATATCGTTGCTCTGTTCCCGAATTATGATAGTAGAAGATATCCAATTCGAACAGTTTCCCAATTAACAAGAGAAATTTATACAAACCCAG
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+  1100
ThrValLeuAspIleValAlaLeuPheProAsnTyrAspSerArgArgTyrProIleArgThrValSerGlnLeuThrArgGluIleTyrThrAsnProV

TATTAGAAAATTTTGATGGTAGTTTTCGAGGCTCGGCTCAGGGCATAGAAAGAAGTATTAGGAGTTCACATTTGATGGATATACTTAACAGTATAACCAT
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+  1200
alLeuGluAsnPheAspGlySerPheArgGlySerAlaGlnGlyIleGluArgSerIleArgSerSerHisLeuMetAspIleLeuAsnSerIleThrIl

CTATACGGATGCTCATAGGGGTTATT~~ATT~~ATTGGTCAGGGCATCAAATAATGGCTTCTCCTGTAGGGTTTTCGGGGCCAGAATTCACTTTTCCGCTATAT
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+  1300
eTyrThrAspAlaHisArgGlyTyrTyrTyrTrpSerGlyHisGlnIleMetAlaSerProValGlyPheSerGlyProGluPheThrPheProLeuTyr

GGAACTATGGGAAATGCAGCTCCACAACAACGTATTGTTGCTCAACTAGGTCAGGGCGTGTATAGAACATTATCGTCCACTTTATATAGAAGACCTTTTA
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+  1400
GlyThrMetGlyAsnAlaAlaProGlnGlnArgIleValAlaGlnLeuGlyGlnGlyValTyrArgThrLeuSerSerThrLeuTyrArgArgProPheA

ATATAGGGATAAATAATCAACAACTATCTGTTCTTGACGGGACAGAATTTGCTTATGGAACCTCCTCAAATTTGCCATCCGCTGTATACAGAAAAAGCGG
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+  1500
snIleGlyIleAsnAsnGlnGlnLeuSerValLeuAspGlyThrGluPheAlaTyrGlyThrSerSerAsnLeuProSerAlaValTyrArgLysSerGl
```

FIG. 1 – 1

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AACCGTAGATTCCCTGGATGAAATACCGCCACAGAATAACAACGTCCCACCTAGGCAAGGATTTAGTCATCGATTAAGCCATGTTTCAATGTTTCGTTCA
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+ 1600
yThrValAspSerLeuAspGluIleProProGlnAsnAsnAsnValProProArgGlnGlyPheSerHisArgLeuSerHisValSerMetPheArgSer
GGCTTTAGTAATAGTAGTGTAAGTATAATAAGAGCTCCTATGTTCTCTTGGATACATCGTAGTGCTGAATTTAATAATATAATTGCATCGGATAGTATTA
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+ 1700
GlyPheSerAsnSerSerValSerIleIleArgAlaProMetPheSerTrpIleHisArgSerAlaGluPheAsnAsnIleIleAlaSerAspSerIleT
CTCAAATCCCTGCAGTGAAGGGAAACTTTCTTTTTAATGGTTCTGTAATTTCAGGACCAGGATTTACTGGTGGGGACTTAGTTAGATTAAATAGTAGTGG
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+ 1800
hrGlnIleProAlaValLysGlyAsnPheLeuPheAsnGlySerValIleSerGlyProGlyPheThrGlyGlyAspLeuValArgLeuAsnSerSerGl
AAATAACATTCAGAATAGAGGGTATATTGAAGTTCCAATTCACTTCCCATCGACATCTACCAGATATCGAGTTCGTGTACGGTATGCTTCTGTAACCCCG
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+ 1900
yAsnAsnIleGlnAsnArgGlyTyrIleGluValProIleHisPheProSerThrSerThrArgTyrArgValArgValArgTyrAlaSerValThrPro
ATTCACCTCAACGTTAATTGGGGTAATTCATCCATTTTTTCCAATACAGTACCAGCTACAGCTACGTCATTAGATAATCTACAATCAAGTGATTTTGGTT
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+ 2000
IleHisLeuAsnValAsnTrpGlyAsnSerSerIlePheSerAsnThrValProAlaThrAlaThrSerLeuAspAsnLeuGlnSerSerAspPheGlyT
ATTTTGAAAGTGCCAATGCTTTTACATCTTCATTAGGTAATATAGTAGGTGTTAGAAATTTTAGTGGGACTGCAGGAGTGATAATAGACAGATTTGAATT
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+ 2100
yrPheGluSerAlaAsnAlaPheThrSerSerLeuGlyAsnIleValGlyValArgAsnPheSerGlyThrAlaGlyValIleIleAspArgPheGluPh
TATTCCAGTTACTGCAACACTCGAGGCTGAATATAATCTGGAAAGAGCGCAGAAGGCGGTGAATGCGCTGTTTACGTCTACAAACCAACTAGGGCTAAAA
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+ 2200
eIleProValThrAlaThrLeuGluAlaGluTyrAsnLeuGluArgAlaGlnLysAlaValAsnAlaLeuPheThrSerThrAsnGlnLeuGlyLeuLys
ACAAATGTAACGGATTATCATATTGATCAAGTGTCCAATTTAGTTACGTATTTATCGGATGAATTTTGTCTGGATGAAAAGCGAGAATTGTCCGAGAAAG
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+ 2300
ThrAsnValThrAspTyrHisIleAspGlnValSerAsnLeuValThrTyrLeuSerAspGluPheCysLeuAspGluLysArgGluLeuSerGluLysV
TCAAACATGCCAAGGCACTCAGTGATGAACGCAATTTACTCCAAGATTCAAATTTCAAAGACATTAATAGGCAACCAGAACGTGGGTGGGGCGGAAGTAC
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+ 2400
alLysHisAlaLysAlaLeuSerAspGluArgAsnLeuLeuGlnAspSerAsnPheLysAspIleAsnArgGlnProGluArgGlyTrpGlyGlySerTh
AGGGATTACCATCCAAGGAGGGGATGACGTATTTAAAGAAAATTACGTCACACTATCAGGTACCTTTGATGAGTGCTATCCAACATATTTGTATCAAAAA
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+ 2500
rGlyIleThrIleGlnGlyGlyAspAspValPheLysGluAsnTyrValThrLeuSerGlyThrPheAspGluCysTyrProThrTyrLeuTyrGlnLys
ATCGATGAATCAAAATTAAAAGCCTTTACCCGTTATCAATTAAGAGGGTATATCGAAGATAGTCAAGACTTAGAAATCTATTTAATTCGCTACAATGCAA
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+ 2600
IleAspGluSerLysLeuLysAlaPheThrArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArgTyrAsnAlaL
AACATGAAACAGTAAATGTGCCAGGTACGGGTTCCTTATGGCCGCTTTCAGCCCAAAGTCCAATCGGAAAGTGTGGAGAGCCGAATCGATGCGCGCCACA
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+ 2700
ysHisGluThrValAsnValProGlyThrGlySerLeuTrpProLeuSerAlaGlnSerProIleGlyLysCysGlyGluProAsnArgCysAlaProHi
CCTTGAATGGAATCCTGACTTAGATTGTTCGTGTAGGGATGGAGAAAAGTGTGCCCATCATTCGCATCATTTCTCCTTAGACATTGATGTAGGATGTACA
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+ 2800
sLeuGluTrpAsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHisHisPheSerLeuAspIleAspValGlyCysThr
GACTTAAATGAGGACCTAGGTGTATGGGTGATCTTTAAGATTAAGACGCAAGATGGGCACGCAAGACTAGGGAATCTAGAGTTTCTCGAAGAGAAACCAT
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+ 2900
AspLeuAsnGluAspLeuGlyValTrpValIlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGluGluLysProL
TAGTAGGAGAAGCGCTAGCTCGTGTCAAAAGAGCGGAGAAAAAATGGAGAGACAAACGTGAAAAATTGGAATGGGAAACAAATATCGTTTATAAAGAGGC
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+ 3000
euValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTrpArgAspLysArgGluLysLeuGluTrpGluThrAsnIleValTyrLysGluAl
AAAAGAATCTGTAGATGCTTTATTTGTAAACTCTCAATATGATCAATTACAAGCGGATACGAATATTGCCATGATTCATGCGGCAGATAAACGTGTTCAT
----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+----,----+ 3100
aLysGluSerValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAlaMetIleHisAlaAlaAspLysArgValHis
AGCATTCGAGAAGCTT
----,----+----,- 3116
SerIleArgGluAlaT
```

FIG. 1 - 2

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Map of pTi15955 T-DNA

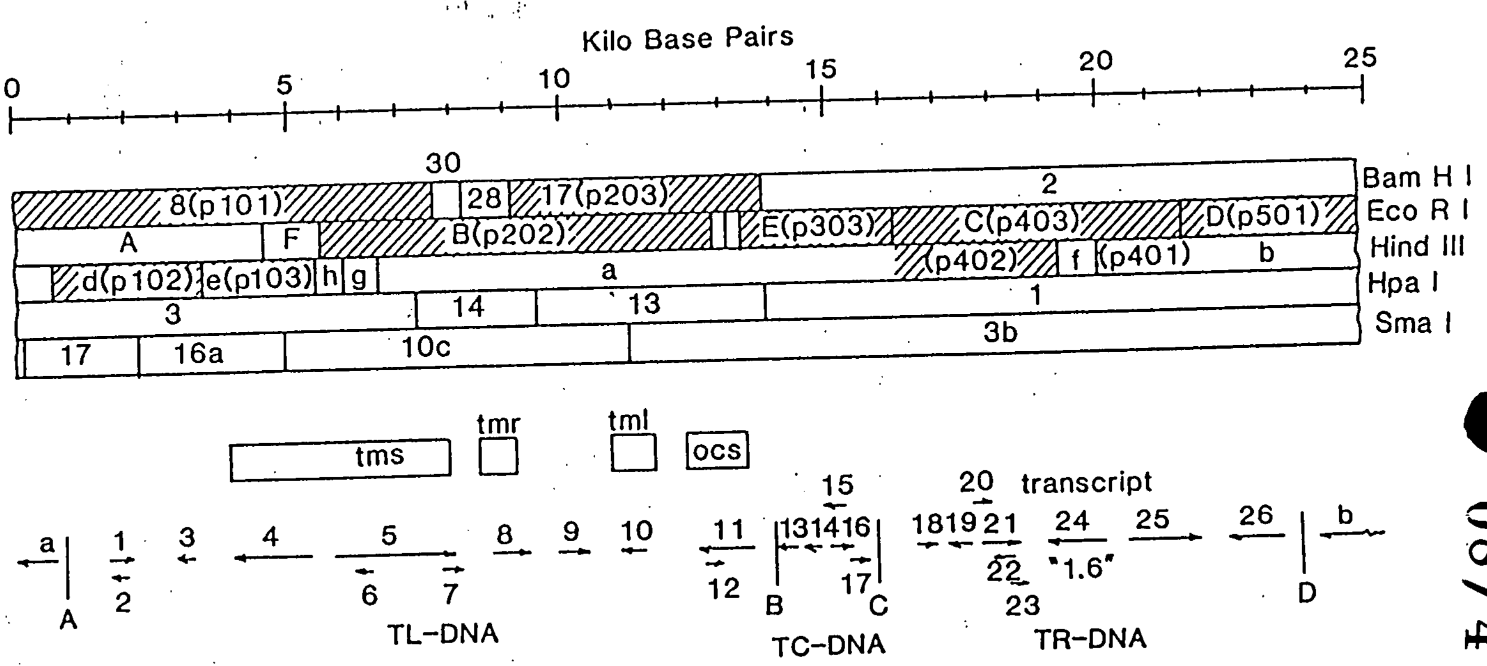

FIG. 2

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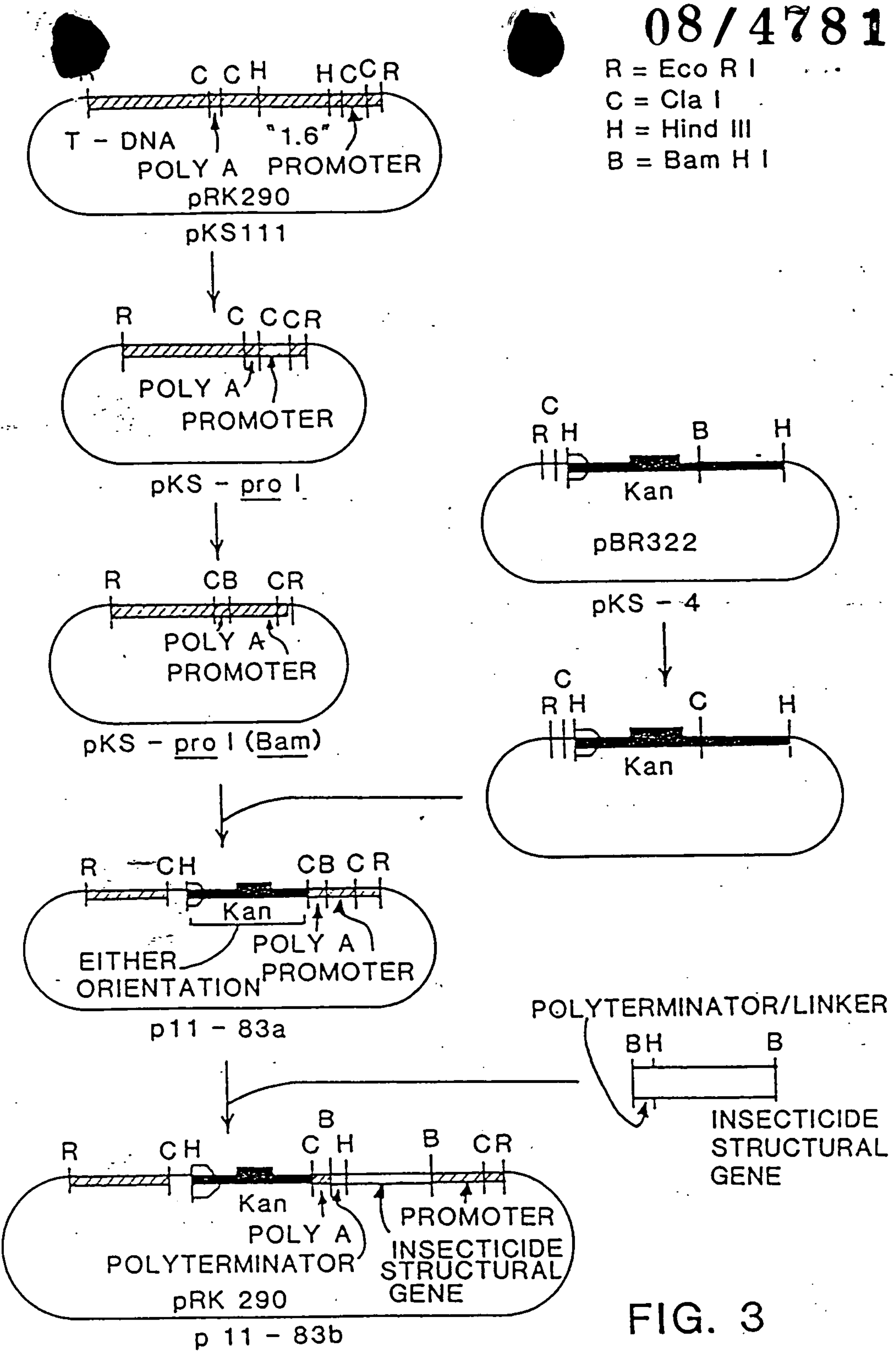

FIG. 3